Amendments to the Specification:

On page 1 of the specification, delete the title starting with "RIBOSOME STRUCTURE" and ending with "INHIBITORS" and replace with the following new title:

-- MODULATORS OF RIBOSOMAL FUNCTION AND IDENTIFICATION THEREOF --

Please amend the first full paragraph appearing on page 30 to read as follows:

-- As used herein, the term "atomic co-ordinates" or "structure co-ordinates" refers to mathematical co-ordinates (represented as "X," "Y" and "Z" values) that describe the positions of atoms in a crystal of a ribosome or ribosomal subunit. The diffraction data obtained from the crystals are used to calculate an electron density map of the repeating unit of the crystal. The electron density maps are used to establish the positions of the individual atoms within a single ribosomal subunit. Those of skill in the art understand that a set of structure co-ordinates determined by X-ray crystallography is not without standard error. For the purpose of this invention, any set of structure co-ordinates for a ribosome or ribosomal subunit from any source has a root mean square deviation of non-hydrogen atoms of less than 0.75 Å when superimposed on the non-hydrogen atom positions of the said atomic co-ordinates deposited at the Research Collaboratory for Structural Bioinformatics (RCSB) Protein Data Bank (PDB) (Berman *et al.* (2000) *Nucleic Acids Research* 28, 235-242; ~~http://www.~~ see also, the web page at the universal resource locator (URL) rcsb.org/pdb/) with the accession numbers PDB ID: 1FFK; PDB ID: 1FFZ; PDB ID: 1FG0; or PDB ID: 1JJ2, the disclosure of each of the foregoing of which is incorporated herein by reference in its entirety. --

Please amend the third full paragraph appearing on page 33 to read as follows:

-- As used herein, the term "homologue" is understood to mean any one or combination of (i) any protein isolated or isolatable from a ribosome or a ribosomal subunit (*i.e.*, a ribosomal protein), (ii) any nucleic acid sequence isolated or isolatable from a ribosome or ribosomal

subunit (*i.e.*, a ribosomal RNA), (iii) any protein having at least 25 % sequence identity to a ribosomal protein isolated from *E. coli* or *Rattus norvegicus* as determined using the computer program "BLAST" version number 2.1.1 implementing all default parameters, or (iv) any nucleic acid having at least 30% sequence identity to a ribosomal RNA isolated from *E. coli* or *Rattus norvegicus* as determined using the computer program "BLAST" version number 2.1.1 implementing all default parameters. "BLAST" version number 2.1.1 is available and accessible via the world wide web at ~~http://www/~~ the URL ncbi.nlm.nih.gov/BLAST/ or can be run locally as a fully executable program on a standalone computer. --

Please amend the first full paragraph appearing on page 37 to read as follows:

-- The present invention is also based, in part, on the atomic structure of the crystal of the 50S ribosomal subunit from *H. marismortui* that has been derived from a 2.4 Å resolution electron density map that was experimentally phased using heavy atom derivatives. The atomic co-ordinates defining the large ribosomal unit were deposited on July 10, 2000, at Research Collaboratory for Structural Bioinformatics (RCSB) Protein Data Bank (PDB) (Berman *et al.* (2000) *Nucleic Acid Research* 28, 235-242; ~~http:// www.~~ see also, the web page at the URL rcsb.org/pdb/) with accession number PDB ID: 1FFK. --

Please amend the first full paragraph appearing on page 53 to read as follows:

-- Analysis of the atomic co-ordinates discussed in section IIA above together with additional atomic co-ordinates of a ribosomal subunit complexed with various analogues, similarly refined, permit an analysis of ribosome function. Accordingly, the present invention is also based on the crystals of *Haloarcula marismortui* 50S ribosomal subunit complexed either with the Yarus transition state analogue, CCdA-p-Puro, or with a mini-helix analogue of an aminoacyl-tRNA. The present invention provides the structures of both complexes. The atomic co-ordinates of the structure of both complexes were deposited on July 26, 2000, at Research Collaboratory for Structural Bioinformatics (RCSB) Protein Data Bank (PDB) (Berman *et al.* (2000) *Nucleic Acid Research* 28: 235-242; ~~http:// www.~~ see also, the web page at the URL rcsb.org/pdb/) with accession numbers PDB ID: 1FFZ (50S ribosome/ CCdA-p-Puro complex) and PDB ID: 1FG0 (50S ribosome/aa-tRNA analogue). --

Please amend the paragraph bridging pages 74 and 75 to read as follows:

-- By way of example, since the nucleotide sequences of all known 50S subunit rRNAs can be aligned relative to each other and to *H. marismortui* 23S and 5S rRNAs, it is possible to construct models of the structures of other 50S ribosomal rRNAs, particularly in the regions of the tunnel and active sites, using the *H. marismortui* structure. Likewise, homologous proteins can also be modeled using similar methodologies. Methods useful for comparative RNA sequence analysis are known in the art and include visual methods and number pattern methods, as well as methods employing chi-square statistics, phylogenetic algorithms, or empirical algorithms. Descriptions of some of the foregoing methods are available, for example, at ~~http://www.~~ on the world wide web at the URL rna.icmb.utexas.edu/; Gutell (1996), "Comparative Sequence Analysis and the Structure of 16S and 23S rRNA," Ribosomal RNA. Structure, Evolution, Processing, and Function in Protein Biosynthesis, (Dahlberg A. and Zimmerman B., eds.) CRC Press. Boca Raton, pp. 111-128; Guttell *et al.* (1993) *Nucl. Acid Res.* 21: 3055 - 3074; Schnare *et al.* (1996) *J. Mol. Biol.* 256: 701-719. Particularly useful visual inspection methods include comparison of a particular position in a *H. marismortui* secondary structure diagram with the residues located at the analogous position on an *E. coli* secondary structure diagram. A software program that is particularly useful in homology modeling includes XALIGN (Wishart, D. *et al.*, (1994) *Cabios* 10: 687-88). See also, U.S. Patent No. 5,884,230. --

On page 85, page 86, page 87, page 91, page 94, page 95, page 96, page 97, page 98, page 99, page 100, page 101 and page 102 amend each occurrence of footnote b) as follows:

-- b) Comparative RNA Web Site URL ~~:http://www.~~rna.icmb.utexas.edu/ --